

SPECIFICATION AMENDMENTS

Please replace the paragraphs beginning on page 10, line 12, with the following rewritten paragraphs:

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FIGURE 7 provides the ~~program flow~~ database management screen in the SPADE™ system;

FIGURE 8 provides the ~~database~~ workspace management screen in the SPADE™ system;

FIGURE 9 provides the ~~workspace management~~ search analysis tools screen in the SPADE™ system;

FIGURE 10 provides the ~~search analysis tools screen in~~ system architecture overview of the SPADE™ system;

FIGURE 11 provides ~~the system architecture overview~~ an example of an application of the SPADE™ system;

FIGURE 12 provides an example of an application of the SPADE™ system; and

FIGURE 13 ~~provides an example of an application of the SPADE™ system; and~~ is the nucleic acid and protein sequence of an INTEGRIN protein isolated using the present invention.

FIGURE 14 ~~is the nucleic acid and protein sequence of an INTEGRIN protein isolated using the present invention.~~

Please replace the paragraph beginning on page 13, line 14 through page 14, line 14,
with the following rewritten paragraph:

The nucleic acid and protein sequences described herein are listed for convenience as follows:

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SEQ ID	integrin beta 1 (INTB1) cDNA sequence from <i>M.</i>
NO.: 1	<i>sexta</i> (see FIGURE 14 13)
SEQ ID	ITGB1 protein sequence for <i>M. sexta</i> (see
NO.: 2	FIGURE 14 13)
SEQ ID	ITGB1 forward *primer 741-781 AAY TTG GAY
NO.: 3	WMT CYH GAR GGW GGY TTB GAT GCY MTH ATG CA
SEQ ID	ITGB1 reverse primer 2358-2339 TCR AAY TTR
NO.: 4	GCA WAY TCC CT
SEQ ID	ITGB1 forward primer 3'-RACE ATC ATT CAA
NO.: 5	ACG GAA CCA GAG
SEQ ID	ITGB1 REV 5' -RACE GTC TCC ACC CTA TTT
NO.: 6	CTT TCT CAC
SEQ ID	ITGB1 forward primer for sequencing TTG TGA
NO.: 7	CGG GAC ACC AAT TA
SEQ ID	ITGB1 reverse primer for sequencing GCA TAC
NO.: 8	ACA TTC ACC GTT GC

*Other primers used included commercially available primers from the Clontech SMART™ cDNA Library Construction Kit (SMART III Oligonucleotide; 5' PCR Primer; CDS III/3' PCR Primer; CDS III/3' TRUN).

Please replace the paragraphs beginning on page 55, line 8 through page 57, line 5, with the following rewritten paragraphs:

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~~An illustration of the main program flow is exemplified in FIGURE 7.~~ The program flow is as follows: A user first logs in and is ~~the~~ then presented with a main menu. The main menu presents four choices: Database Management (FIGURE 8 7), Workspace Management (FIGURE 9 8), Search Tools and Analysis Tools (FIGURE 10 9). The Database Management screen allows the administrator of the system to conFIGURE the local genomic databases associated with SPADE™. In this screen, there is a list of current databases online, a button to edit the configuration for each individual database, and options to add new databases or delete existing ~~existing~~ databases. The Workspace Management screen allows the user to access his or her data, files and documentation on the server. It is similar to a file management program. There is a list of projects, and the files in the current project. The user can open a project, create new projects or delete existing projects. Within each project, the user can open individual data files, rename, delete, upload or download files. The search tool screen allows the user to search databases with the algorithms associated with SPADE™. The user first selects the database via a database selection window, and then selects the sequence to search from the project files or enters the sequence directly into the text box. The user then selects the algorithm to search, and accepts the default parameters or modifies the appropriate parameters. Users can access the advance parameters via the advance parameters screen. Finally, the server executes the search and returns the result to the user. The search tool screen also allows the user to analyze the results of the previous search or analysis with the algorithms associated with SPADE™. The user first selects the sequence to analyze from the project files or enters the sequence directly into the text box. The user then selects the algorithm to execute, and accepts the default parameters or modifies the appropriate parameters. Users can access the advance parameters via the advance parameters screen. Finally, the server executes the algorithm and returns the result to the user.

An example of the system architecture overview is illustrated in FIGURE 11 10, showing the interaction of the platform-free users with the four screens discussed above. FIGURE 12 11 describes a use of the system described in FIGURE 11 10. A mere specific example of the application is outlined in FIGURE 13 12, which shows one possible use of the SPADE™ system.

Please replace the paragraph on page 60, lines 11-17, with the following rewritten

paragraph:

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The insert from these clones was then used to clone the full-length cDNA from a *M. sexta* library. The sequence of integrin beta 1 (ITGB1) gene is depicted in FIGURE 44 13 as SEQ ID NO.:1 and the corresponding amino acid sequence is at SEQ ID NO.: 2. These sequences represent preliminary sequence data and the sequences will be completed and confirmed by methods known in the art.
